

Serial Number: 10/044,901

 Changed a file from non-ASCII to ASCII Changed the margins in cases where the sequence text was "wrapped" down to the next line. Edited a format error in the Current Application Data section, specifically:**ENTERED** Edited the Current Application Data section with the actual current number. The number inputted by the applicant was  the prior application data; or  other \_\_\_\_\_. Added the mandatory heading and subheadings for "Current Application Data". Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer. Changed the spelling of a mandatory field (the headings or subheadings), specifically: Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted:  non-ASCII "garbage" at the beginning/end of files;  secretary initials/filename at end of file;  page numbers throughout text;  other invalid text, such as \_\_\_\_\_. Inserted mandatory headings, specifically: Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_. Other:  
\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/044,901

DATE: 02/19/2002  
TIME: 10:56:33

Input Set : A:\PTO\_MS.txt  
Output Set: N:\CRF3\02192002\J044901.raw

ENTERED

4 <110> APPLICANT: Curtis, Rory A.J.  
6 <120> TITLE OF INVENTION: 58297, AN AMINO ACID TRANSPORTER AND  
7 USES THEREFOR  
9 <130> FILE REFERENCE: MPI2001-010P1R(M)  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/044,901  
C--> 11 <141> CURRENT FILING DATE: 2002-01-10  
11 <150> PRIOR APPLICATION NUMBER: 60/262,515  
W--> 12 <151> PRIOR FILING DATE: 2001-1-18  
14 <160> NUMBER OF SEQ ID NOS: 8  
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
18 <210> SEQ ID NO: 1  
19 <211> LENGTH: 2476  
20 <212> TYPE: DNA  
21 <213> ORGANISM: Homo sapiens  
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24 <221> NAME/KEY: -5'UTR  
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27 <221> NAME/KEY: CDS  
28 <222> LOCATION: (128)...(1810)  
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35 tccaccgagt tggagaaacc tactcaacac caggactaac ttcttcagtg ctttagagtgt 120  
36 gagaaaa atg gca aat atg aat agt gat tct agg cat ctt ggc acc tct 169  
37 Met Ala Asn Met Asn Ser Asp Ser Arg His Leu Gly Thr Ser  
38 1 5 10  
40 gag gta gat cat gaa aga gat cct gga cct atg aat atc cag ttt gag 217  
41 Glu Val Asp His Glu Arg Asp Pro Gly Pro Met Asn Ile Gln Phe Glu  
42 15 20 25 30  
44 cca tcg gat cta aga tcc aaa agg cct ttc tgt ata gag ccc aca aac 265  
45 Pro Ser Asp Leu Arg Ser Lys Arg Pro Phe Cys Ile Glu Pro Thr Asn  
46 35 40 45  
48 atc gtg aat gtg aat cat gtc att cag agg gtt agt gac cat gcc tct 313  
49 Ile Val Asn Val Asn His Val Ile Gln Arg Val Ser Asp His Ala Ser  
50 50 55 60  
52 gcc atg aac aag aga att cat tac tac agc cgg ctc acc act cct gca 361  
53 Ala Met Asn Lys Arg Ile His Tyr Tyr Ser Arg Leu Thr Thr Pro Ala  
54 65 70 75  
56 gac aag gca ctg att gcc cca gac cat gta gtt cca gct cca gaa gag 409  
57 Asp Lys Ala Leu Ile Ala Pro Asp His Val Val Pro Ala Pro Glu Glu  
58 80 85 90  
60 tgc tat gtg tat agt cca ttg ggc tct gct tat aaa ctt caa agt tac 457

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61	Cys	Tyr	Val	Tyr	Ser	Pro	Leu	Gly	Ser	Ala	Tyr	Lys	Leu	Gln	Ser	Tyr	
62	95										100		105			110	
64	act	gaa	gga	tac	ggt	aaa	aac	acc	agt	tta	gta	acc	att	ttt	atg	att	505
65	Thr	Glu	Gly	Tyr	Gly	Lys	Asn	Thr	Ser	Leu	Val	Thr	Ile	Phe	Met	Ile	
66										115		120			125		
68	tgg	aat	acc	atg	atg	gga	aca	tct	ata	cta	agc	att	cct	tgg	ggc	ata	553
69	Trp	Asn	Thr	Met	Met	Gly	Thr	Ser	Ile	Leu	Ser	Ile	Pro	Trp	Gly	Ile	
70									130		135			140			
72	aaa	cag	gct	gga	ttt	act	act	gga	atg	tgt	gtc	atc	ata	ctg	atg	ggc	601
73	Lys	Gln	Ala	Gly	Phe	Thr	Thr	Gly	Met	Cys	Val	Ile	Ile	Leu	Met	Gly	
74									145		150			155			
76	ctt	tta	aca	ctt	tat	tgc	tgc	tac	aga	gta	gtg	aaa	tca	cg	act	atg	649
77	Leu	Leu	Thr	Leu	Tyr	Cys	Cys	Tyr	Arg	Val	Val	Lys	Ser	Arg	Thr	Met	
78									160		165			170			
80	atg	ttt	tca	ttg	gat	acc	act	acc	tgg	gaa	tat	cca	gat	gtc	tgc	aga	697
81	Met	Phe	Ser	Leu	Asp	Thr	Thr	Trp	Glu	Tyr	Pro	Asp	Val	Cys	Arg		
82	175								180			185			190		
84	cat	tat	ttc	ggc	tcc	ttt	ggg	cag	tgg	tgc	agt	ctc	ctc	ttc	tcc	ttg	745
85	His	Tyr	Phe	Gly	Ser	Phe	Gly	Gln	Trp	Ser	Ser	Leu	Leu	Phe	Ser	Leu	
86									195			200			205		
88	gtg	tct	ctc	att	gga	gca	atg	ata	gtt	tat	tgg	gtg	ctt	atg	tca	aat	793
89	Val	Ser	Leu	Ile	Gly	Ala	Met	Ile	Val	Tyr	Trp	Val	Leu	Met	Ser	Asn	
90									210		215			220			
92	ttt	ctt	ttt	aat	act	gga	aag	ttt	att	ttt	aat	ttt	att	cat	cac	att	841
93	Phe	Leu	Phe	Asn	Thr	Gly	Lys	Phe	Ile	Phe	Asn	Phe	Ile	His	His	Ile	
94									225		230			235			
96	aat	gac	aca	gac	act	ata	ctg	agt	acc	aat	aat	agc	aac	cct	gtg	att	889
97	Asn	Asp	Thr	Asp	Thr	Ile	Leu	Ser	Thr	Asn	Asn	Ser	Asn	Pro	Val	Ile	
98									240		245			250			
100	tgt	cca	agt	gcc	ggg	agt	gga	ggc	cat	cct	gac	aac	agc	tct	atg	att	937
101	Cys	Pro	Ser	Ala	Gly	Ser	Gly	Gly	His	Pro	Asp	Asn	Ser	Ser	Met	Ile	
102	255								260			265			270		
104	ttc	tat	gcc	aat	gac	aca	gga	gcc	caa	cag	ttt	gaa	aag	tgg	tgg	gat	985
105	Phe	Tyr	Ala	Asn	Asp	Thr	Gly	Ala	Gln	Gln	Phe	Glu	Lys	Trp	Trp	Asp	
106									275			280			285		
108	aag	tcc	agg	aca	gtc	ccc	ttt	tat	ctt	gta	ggg	ctc	ctc	ctc	cca	ctg	1033
109	Lys	Ser	Arg	Thr	Val	Pro	Phe	Tyr	Leu	Val	Gly	Leu	Leu	Leu	Pro	Leu	
110									290		295			300			
112	ctc	aat	ttc	aag	tct	cct	tca	ttt	tca	aaa	ttt	aat	atc	cta	ggc		1081
113	Leu	Asn	Phe	Lys	Ser	Pro	Ser	Phe	Phe	Ser	Lys	Phe	Asn	Ile	Leu	Gly	
114									305		310			315			
116	aca	gtg	tct	gtc	ctt	tat	ttg	att	ttc	ctt	gtc	acc	ttt	aag	gct	gtt	1129
117	Thr	Val	Ser	Val	Leu	Tyr	Leu	Ile	Phe	Leu	Val	Thr	Phe	Lys	Ala	Val	
118									320		325			330			
120	cgc	ttg	gga	ttt	cat	ttg	gaa	ttt	cat	tgg	ttt	ata	cca	aca	gaa	ttt	1177
121	Arg	Leu	Gly	Phe	His	Leu	Glu	Phe	His	Trp	Phe	Ile	Pro	Thr	Glu	Phe	
122	335								340			345			350		1225
124	ttt	gta	cca	gag	ata	aga	ttt	cag	ttt	cca	cag	ctg	act	gga	gtg	ctt	
125	Phe	Val	Pro	Glu	Ile	Arg	Phe	Gln	Phe	Pro	Gln	Leu	Thr	Gly	Val	Leu	

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126	355	360	365		
128	acc ctt gct ttt ttt att cat aat tgt atc atc aca ctc ttg aag aac			1273	
129	Thr Leu Ala Phe Phe Ile His Asn Cys Ile Ile Thr Leu Leu Lys Asn				
130	370	375	380		
132	aac aag aaa caa gaa aac aat gtg agg gac ttg tgc att gct tat atg			1321	
133	Asn Lys Lys Gln Glu Asn Asn Val Arg Asp Leu Cys Ile Ala Tyr Met				
134	385	390	395		
136	ctg gtg aca tta act tat ctc tat att gga gtc ctg gtt ttt gct tca			1369	
137	Leu Val Thr Leu Thr Tyr Ile Gly Val Leu Val Phe Ala Ser				
138	400	405	410		
140	ttt cct tca cca cca tta tcc aaa gat tgt att gag cag aat ttt tta			1417	
141	Phe Pro Ser Pro Pro Leu Ser Lys Asp Cys Ile Glu Gln Asn Phe Leu				
142	415	420	425	430	1465
144	gac aac ttc cct agc agt gac acc ctg tcc att gca agg ata ttc				
145	Asp Asn Phe Pro Ser Ser Asp Thr Leu Ser Phe Ile Ala Arg Ile Phe				
146	435	440	445		
148	ctg ctg ttc cag atg atg act gta tac cca ctc tta ggc tac ctg gct			1513	
149	Leu Leu Phe Gln Met Met Thr Val Tyr Pro Leu Leu Gly Tyr Leu Ala				
150	450	455	460		
152	cgt gtc cag ctt ttg ggc cat atc ttc ggt gac att tat cct agc att			1561	
153	Arg Val Gln Leu Leu Gly His Ile Phe Gly Asp Ile Tyr Pro Ser Ile				
154	465	470	475		
156	ttc cat gtg ctg gtt ctt aat cta att att gtg gga gct gga gtg atc			1609	
157	Phe His Val Leu Val Leu Asn Leu Ile Ile Val Gly Ala Gly Val Ile				
158	480	485	490		
160	atg gcc tgt ttc tac cca aac ata gga ggg atc ata aga tat tca gga			1657	
161	Met Ala Cys Phe Tyr Pro Asn Ile Gly Ile Ile Arg Tyr Ser Gly				
162	495	500	505	510	1705
164	gca gca tgt gga ctg gcc ttt gta ttc ata tac cca tct ctc atc tat				
165	Ala Ala Cys Gly Leu Ala Phe Val Phe Ile Tyr Pro Ser Leu Ile Tyr				
166	515	520	525		
168	ata att tcc ctc cac caa gaa gag cgt ctg aca tgg cct aaa tta atc			1753	
169	Ile Ile Ser Leu His Gln Glu Glu Arg Leu Thr Trp Pro Lys Leu Ile				
170	530	535	540		
172	ttc cac gtt ttc atc atc att ttg ggc gtg gct aac ctg att gtt cag			1801	
173	Phe His Val Phe Ile Ile Leu Gly Val Ala Asn Leu Ile Val Gln				
174	545	550	555		
176	ttt ttt atg tgaaatacct caactgtttt ttcaagagc tctcatgata			1850	
177	Phe Phe Met				
178	560				
180	ttttgaggct tgacaacagt tctatataaa ttcaacttgc aatgctgtgt ttgtgtatt			1910	
181	ctaaatattt tctaagataa ttgaaagca agggaaatag tggccctta atgagtattt			1970	
182	ttttatttggg gtggggaaag gggcaaaaag aatgatctta gtgtcttaac ctttctcata			2030	
183	ttaactcacc tctttattct gtggtcttt ctgaatagaa atgtatgccc taggaagaaa			2090	
184	tcatgctggg tttgtctttt agagataaaa ggtgggtggat ttatggcc tgcatgtaaag			2150	
185	attctcaggg tgtcagagca gcatattgtc aaatcctgct tctgtttat gttcagtgt			2210	
186	attcacttcc atttcttac ttactagacc atttctgcag ttggccaaa cctctactgt			2270	
187	ttgggacagt aagccaaata cctcatttt aaaaagaagt ttcatggca tcagtgttaa			2330	
188	taaagtacat ttttaactga gtcttaatct ctatggaa aaaaagtaga gacaaaagta			2390	

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193 <211> LENGTH: 561  
194 <212> TYPE: PRT  
195 <213> ORGANISM: Homo sapiens  
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200 Asp His Glu Arg Asp Pro Gly Pro Met Asn Ile Gln Phe Glu Pro Ser  
201 20 25 30  
202 Asp Leu Arg Ser Lys Arg Pro Phe Cys Ile Glu Pro Thr Asn Ile Val  
203 35 40 45  
204 Asn Val Asn His Val Ile Gln Arg Val Ser Asp His Ala Ser Ala Met  
205 50 55 60  
206 Asn Lys Arg Ile His Tyr Tyr Ser Arg Leu Thr Thr Pro Ala Asp Lys  
207 65 70 75 80  
208 Ala Leu Ile Ala Pro Asp His Val Val Pro Ala Pro Glu Glu Cys Tyr  
209 85 90 95  
210 Val Tyr Ser Pro Leu Gly Ser Ala Tyr Lys Leu Gln Ser Tyr Thr Glu  
211 100 105 110  
212 Gly Tyr Gly Lys Asn Thr Ser Leu Val Thr Ile Phe Met Ile Trp Asn  
213 115 120 125  
214 Thr Met Met Gly Thr Ser Ile Leu Ser Ile Pro Trp Gly Ile Lys Gln  
215 130 135 140  
216 Ala Gly Phe Thr Thr Gly Met Cys Val Ile Ile Leu Met Gly Leu Leu  
217 145 150 155 160  
218 Thr Leu Tyr Cys Cys Tyr Arg Val Val Lys Ser Arg Thr Met Met Phe  
219 165 170 175  
220 Ser Leu Asp Thr Thr Trp Glu Tyr Pro Asp Val Cys Arg His Tyr  
221 180 185 190  
222 Phe Gly Ser Phe Gly Gln Trp Ser Ser Leu Leu Phe Ser Leu Val Ser  
223 195 200 205  
224 Leu Ile Gly Ala Met Ile Val Tyr Trp Val Leu Met Ser Asn Phe Leu  
225 210 215 220  
226 Phe Asn Thr Gly Lys Phe Ile Phe Asn Phe Ile His His Ile Asn Asp  
227 225 230 235 240  
228 Thr Asp Thr Ile Leu Ser Thr Asn Asn Ser Asn Pro Val Ile Cys Pro  
229 245 250 255  
230 Ser Ala Gly Ser Gly Gly His Pro Asp Asn Ser Ser Met Ile Phe Tyr  
231 260 265 270  
232 Ala Asn Asp Thr Gly Ala Gln Gln Phe Glu Lys Trp Trp Asp Lys Ser  
233 275 280 285  
234 Arg Thr Val Pro Phe Tyr Leu Val Gly Leu Leu Leu Pro Leu Leu Asn  
235 290 295 300  
236 Phe Lys Ser Pro Ser Phe Phe Ser Lys Phe Asn Ile Leu Gly Thr Val  
237 305 310 315 320  
238 Ser Val Leu Tyr Leu Ile Phe Leu Val Thr Phe Lys Ala Val Arg Leu  
239 325 330 335

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240 Gly Phe His Leu Glu Phe His Trp Phe Ile Pro Thr Glu Phe Phe Val  
241 340 345 350  
242 Pro Glu Ile Arg Phe Gln Phe Pro Gln Leu Thr Gly Val Leu Thr Leu  
243 355 360 365  
244 Ala Phe Phe Ile His Asn Cys Ile Ile Thr Leu Leu Lys Asn Asn Lys  
245 370 375 380  
246 Lys Gln Glu Asn Asn Val Arg Asp Leu Cys Ile Ala Tyr Met Leu Val  
247 385 390 395 400  
248 Thr Leu Thr Tyr Leu Tyr Ile Gly Val Leu Val Phe Ala Ser Phe Pro  
249 405 410 415  
250 Ser Pro Pro Leu Ser Lys Asp Cys Ile Glu Gln Asn Phe Leu Asp Asn  
251 420 425 430  
252 Phe Pro Ser Ser Asp Thr Leu Ser Phe Ile Ala Arg Ile Phe Leu Leu  
253 435 440 445  
254 Phe Gln Met Met Thr Val Tyr Pro Leu Leu Gly Tyr Leu Ala Arg Val  
255 450 455 460  
256 Gln Leu Leu Gly His Ile Phe Gly Asp Ile Tyr Pro Ser Ile Phe His  
257 465 470 475 480  
258 Val Leu Val Leu Asn Leu Ile Ile Val Gly Ala Gly Val Ile Met Ala  
259 485 490 495  
260 Cys Phe Tyr Pro Asn Ile Gly Gly Ile Ile Arg Tyr Ser Gly Ala Ala  
261 500 505 510  
262 Cys Gly Leu Ala Phe Val Phe Ile Tyr Pro Ser Leu Ile Tyr Ile Ile  
263 515 520 525  
264 Ser Leu His Gln Glu Glu Arg Leu Thr Trp Pro Lys Leu Ile Phe His  
265 530 535 540  
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267 545 550 555 560  
268 Met  
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273 <211> LENGTH: 1683  
274 <212> TYPE: DNA  
275 <213> ORGANISM: Homo sapiens  
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278 <221> NAME/KEY: CDS  
279 <222> LOCATION: (1)...(1683)  
281 <400> SEQUENCE: 3  
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284 1 5 10 15  
286 gat cat gaa aga gat cct gga cct atg aat atc cag ttt gag cca tcg 96  
287 Asp His Glu Arg Asp Pro Gly Pro Met Asn Ile Gln Phe Glu Pro Ser  
288 20 25 30  
290 gat cta aga tcc aaa agg cct ttc tgt ata gag ccc aca aac atc gtg 144  
291 Asp Leu Arg Ser Lys Arg Pro Phe Cys Ile Glu Pro Thr Asn Ile Val  
292 35 40 45  
294 aat gtg aat cat gtc att cag agg gtt agt gac cat gcc tct gcc atg 192  
295 Asn Val Asn His Val Ile Gln Arg Val Ser Asp His Ala Ser Ala Met  
296 50 55 60

VERIFICATION SUMMARY  
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Input Set : A:\PTO\_MS.txt  
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:12 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD